STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/562,383_
Source: _IFWP_
Date Processed by STIC: _1/9/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> **http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual - ePAVE**)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: *10/562,383*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
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9____Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213> Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220>

Sequence(s)_____missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa

"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFWP

RAW SEQUENCE LISTING   DATE: 01/09/2006
PATENT APPLICATION: US/10/562,383   TIME: 11:39:50

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Output Set: N:\CRF4\01092006\J562383.raw

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C--> 10 <141> CURRENT FILING DATE: 2005-12-23
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     28 <151> PRIOR FILING DATE: 2004-02-27
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216 gccggaaggt gcgagttagt gcgctcgatt gtgggcgggg gcggaaagag gcgcgtttta   720
217 aagtggtaac agatggtttt cttatccaat aggattaaaa aatttgtcct tacccggccg   780
218 accgcggaag tagagtaggc gggcggccaa tggggacatg atgggggggcg gagccgaggc   840
219 ctccgaagcg gaagtgggtt gctgttgagg cggcggcatc tttctcgagg agctctcctg   900
220 ggcggctgaa gaaggagctt cttctccgga gtgcgccggc ggtggcgcct gcggacctaa   960
221 ctagctccag gttaggccga gctttgcggg aaagcagcgg taagtcaggg ccttgcagat  1020
222 gcgaggttta ggcagcttcg cggcctacag aggcctcggc ccgcgcctct tgggggagcc  1080
223 gcgctgcgcg gcttgaccca gccgaggctt tgcagcccgg gacctcgagc cagctctggt  1140
224 cgctcgcact gccgtccgcg cgggcgcacc gagcccggct tggcgcgggc aacagaagtt  1200
225 aggaggtctg cgtctgggtc tcggctcacc ctgggggggcc gcggccatgg ggcttagttc  1260
226 ctagcctagg aagggaaact gagactctgg gaggggcagg aacgcccca aggtcacttg  1320
227 gaaagtcggg caggatgtgc tgttagggggg aagacccggg cagggttttt gttccccgct  1380
228 gacgacgcct cctttgtgtg ttcgcgccgc cgccccgcca tcgtggggcc tgcgagtttg  1440
229 ccggggtgcg tgggccgcgt ggcggggcct tttgtaggtc gggaggatct gagtacgggt  1500
230 gcgggcctga ccgtgggggc gccgaggtcg cagtctaaaa cttagtaggg cctcgatttc  1560
231 cgggcgcgct tccgggcccc ggctggtggt tggtggaacg tgcgactgtg aggcttgcgg  1620
232 cccagccctg caccgctcgg gcccttcacc gctctggcgc gcctatagac aggtgtatga  1680
233 agattctcac gacccgaaac agagttgcta gtaaacaccg cttttccgcc tttgatccat  1740
234 cggggaagag ggaaaaggat agagcttggg caagccgttt tggtagggat ttcagctttt  1800
235 gtctttcact tgtcagttcc catagacgtt cacaaactta ataatcttcg ttctgtttct  1860
236 gcaccaagtt cttgagccag acgtagggtc tcagctctgg agcctggctt agactgtcca  1920
237 actgactggg gagactgagg tccagaaaag tgaagtggtc tgcccaaggt cacatagcca  1980
238 gctatttggc agcagatgag gttaagtcct acctgcaaga tttgggtttt gaattcattg  2040
239 accaggagtt ttgggaccac tgtcaataaa agagacattg aagggaatct tttgttactt  2100
240 tcttggtgat ttgctttta atggacaagg acatattggg ttcagtttta tctgtgagtt  2160
241 tgaggtgaaa tagaggcatt cgagtagcaa gatatattgc tggcttttgt attgcctgaa  2220
242 tttgagcttc caaaaatctt actttaacac atcgtttatt gatctttct tgaattacta  2280
243 cctttgtaag gacctttgt aaacattgtt tttctaatct tcatgaaatc ttaatgccat  2340
244 acgtaaacta tttctttta tataatgtat gcacatctgt gctttgtaca taaaatgagt  2400
245 aagattt                                                            2407
247 <210> SEQ ID NO: 5
248 <211> LENGTH: 2229
249 <212> TYPE: DNA
250 <213> ORGANISM: Homo Sapiens
252 <400> SEQUENCE: 5
254 tctttcctcg gcgctggctg gtgcgggttg gggtcaggtg gagaagccgc tctttgttaa    60
255 ggtgacagaa cgtgctgggg gtgggggccg gggccagggc cggtgcaact aggggggccgc   120
256 tgcccttttcc tggacacagt ggaagcttct tccgcatcac caaattttttg tcatcctttc   180
257 tgagggacct gcttccaggc agcacgcaag ttgttgtccc gggtttactc cgcacccctc   240
258 tactgggtga ggaaggagca tcttgaatgg agatggggggt gtccccggtt tatacatctg   300
259 cagagaagag gtgtgccggg ctgcacctct ggaggccgcg gtaactgata ttagagaaga   360
260 ccccggttgc agctgggaag gctcactggc tggaaagagg tgcctcctcc ttccagcaaa   420
261 gggccctgtt tggaagggct gcttctcacc tgtctagtgg caccacagga cggtcggctt   480
262 ccactcgaat tcccccggac ggtatcatca catagccggg tcctcgcagt gttggtttcc   540
263 caatccgatg actgtcacct cggtgaggac ctgtgctgat ggccggagaa ccctcgcctg   600
264 cgggcgcaca tggccaggtg gcgcctggca ggcgacgtcc gggtgcagga cggcgctctt   660
```

<210> 674

<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> ← *needs explanation on <223? line. Give source of genetic material (see item 11 on Error Summary Sheet)*

<400> 674

gtatgtagtt gtgtgtt

<210> 675
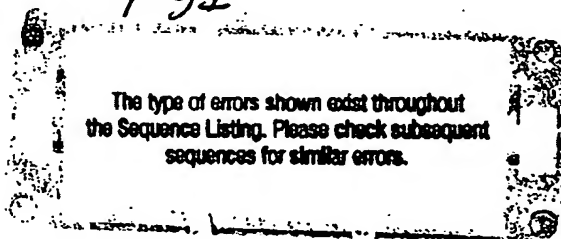<211> 18
<212> DNA
<213> (Artificial Sequence) *same error*

<220>
<223>

<400> 675

tttgagtatt cgtaggaa

The above sequences are samples of global errors

FYI

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

17

18

<210> 1160
<211> 22
<212> DNA
<213> Artificial Sequence

<220> (bisulfite treated)
<223> nucleic acid for analysis of methylation status of SEQ ID NO: 41
<400> 1160
GAGATTGGAG TTTAATTTTG GA   22

<2207 NEVER *has a response. It is a "leader" only. Move this response to <2237 line*

change these letters to lower-case. All nucleotide sequences need to show lower-case letters for the nucleotides

The above is a sample of global errors.

↓

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/09/2006
PATENT APPLICATION: US/10/562,383   TIME: 11:39:51

Input Set : N:\DA\PTO.DA.txt
Output Set: N:\CRF4\01092006\J562383.raw

FYI

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the
<220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:51; N Pos. 2126,2128,2131,2132
Seq#:404; N Pos. 2126,2128,2131,2132
Seq#:405; N Pos. 113,114,117,119
Seq#:520; N Pos. 2126,2128,2131,2132
Seq#:521; N Pos. 113,114,117,119